Early Journal Content on JSTOR, Free to Anyone in the World

This article is one of nearly 500,000 scholarly works digitized and made freely available to everyone in the world by JSTOR.

Known as the Early Journal Content, this set of works include research articles, news, letters, and other writings published in more than 200 of the oldest leading academic journals. The works date from the mid-seventeenth to the early twentieth centuries.

We encourage people to read and share the Early Journal Content openly and to tell others that this resource exists. People may post this content online or redistribute in any way for non-commercial purposes.

Read more about Early Journal Content at http://about.jstor.org/participate-jstor/individuals/early-journal-content.

JSTOR is a digital library of academic journals, books, and primary source objects. JSTOR helps people discover, use, and build upon a wide range of content through a powerful research and teaching platform, and preserves this content for future generations. JSTOR is part of ITHAKA, a not-for-profit organization that also includes Ithaka S+R and Portico. For more information about JSTOR, please contact support@jstor.org.

Mr. W. E. Edington, graduate student in the University of Illinois, directed my attention to the desirability of a study of the given general equations as regards commutative operators with a view to simplifying the treatment of the generalized polyhedron groups.

MODEL OF THE LINKAGE SYSTEM OF ELEVEN SECOND CHROMOSOME GENES OF DROSOPHILA

BY W. E. CASTLE

BUSSEY INSTITUTION, HARVARD UNIVERSITY

Communicated December 26, 1919

In previous papers[1] reasons have been given for thinking the spatial relations of genes to be three-dimensional rather than linear as assumed in the hypothesis of Morgan and his colleagues. In particular it has been shown that in models made to represent the spatial relations of the genes in the sex chromosomes of two different species of Drosophila, using the original unmodified data, as reported by Morgan and Bridges[2] and by Metz,[3] the arrangement is apparently three-dimensional. Recently data have become available for modeling in a similar way the interrelations of the genes in the so-called "second chromosome" of Drosophila ampelophila.[4] Two views of such a model are seen in figures 1 and 2. The model shows the linkage relations of eleven genes, those for which the data are most complete and reliable according to Bridges and Morgan. The data are taken from table 140 of the publication mentioned. Each gene is represented in the model by a small ring of wire and it is connected with another gene by a wire as long in inches as is the cross-over value, in per cent, between the two genes joined by the wire. In the figures the model is suspended by S, the view shown in figure 2 being taken at right angles to that shown in figure 1. The eleven genes represented in the model are as follows:

S, star (0.0)
Sk, streak (15.4)
d, dachs (29.0)
b, black (46.5)
pr, purple (52.7)
vg, vestigial (65.0)
c, curved (73.5)
px, plexus (96.2)
a, arc (98.4)
sp, speck (105.1)
mr, morula (106.3)

The numbers in parentheses indicate the position of each gene in the linear "map" of Bridges and Morgan (p. 127). It will be observed that seven of the genes in this list are represented in the "map" at distances greater than 50 from star, which lies at 0. In the previous publications already cited, I have maintained that since cross-over percentages of 50 or more have not in any case been observed and are logically impossible as a result of linkage, map distances should not be shown in excess of 50. But further consideration of the matter leads me to withdraw this objection. If the arrangement of the genes is really linear, as assumed by Morgan, then double crossing-over is a sufficient explanation of why cross-over percentages do not increase as fast as map distances. But double crossing-over is the questionable phenomenon which need not be assumed if the arrangement is non-linear. Hence, by constructing models such as are shown in figures 1 and 2, I have attempted to ascertain whether a workable system could be found which was able to dispense with double cross-overs, assuming a non-linear arrangement. It seemed to me that such was the case even after the model seen in figures 1 and 2 had been constructed. I next examined the data given by Gowen[5] for the linkage relations of eight genes of the "third chromosome" of Drosophila. On constructing a model to show the spatial relations of the genes, without assuming the arrangement to be linear, and without making any allowances for double or triple crossing-over, I obtained a figure strikingly similar to

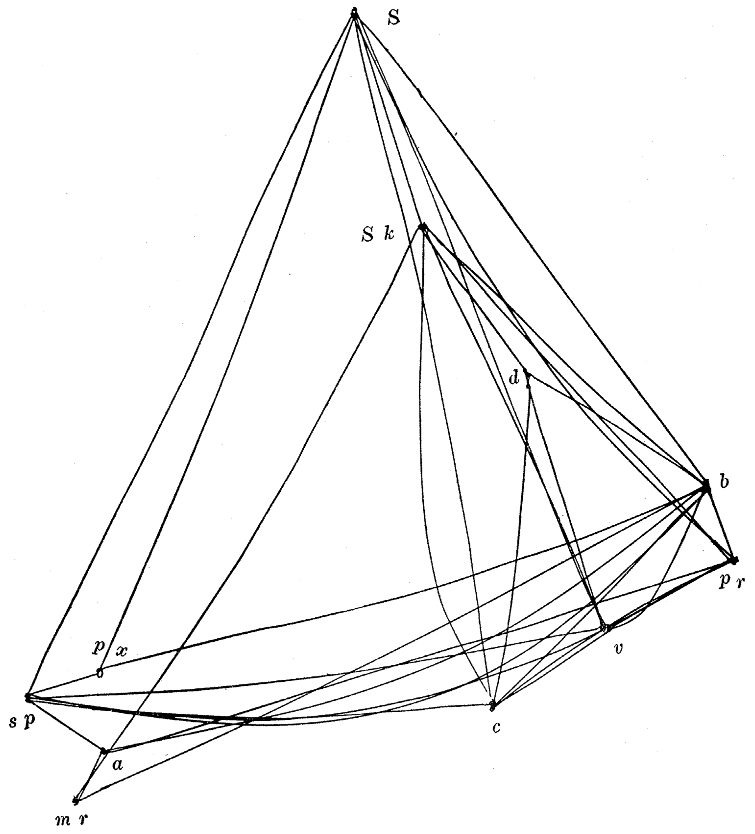

FIG. 1

the model of the sex-linked group of genes. The eight genes fell into a curved band lying nearly in one plane, the model being quite flat as viewed edgewise. The figure indeed is, as Sturtevant, Bridges and Morgan[6] said concerning my model of the sex-chromosome linkage system, "capable

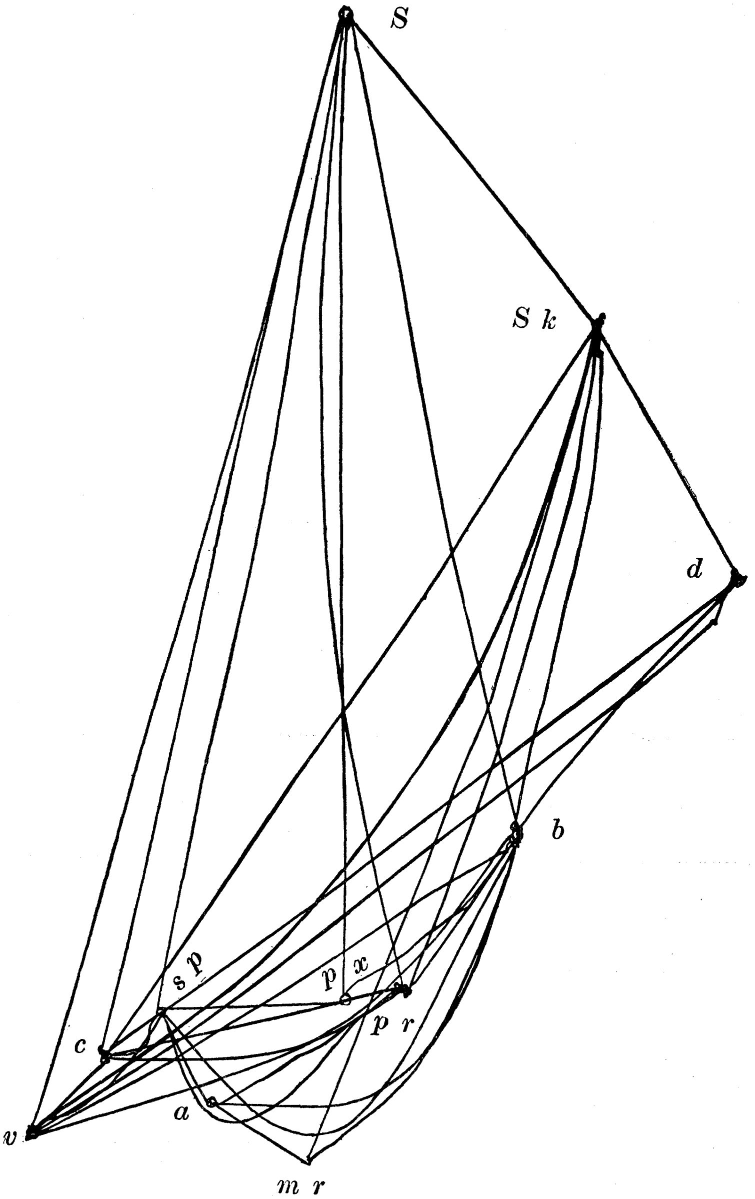

FIG. 2

of reduction to a curved line lying in one plane." Obviously the arrangement approaches the linear, but it is curvilinear rather than rectilinear as shown in the chromosome maps. But if we grant that the arrangement is in any sense linear, then it must be granted also that double and triple crossing-over are likely to occur, indeed we cannot in that case reasonably explain the observed regrouping of characters on any other assumptions. But if double crossing-over occurs oftenest when long distances are involved, it follows that the long distances will have been apparently shortened. If now in the model based on Gowen's observations, we lengthen the long distances by counting twice each assumed double cross-over and thrice each assumed triple cross-over, we do in fact obtain a distribution of the eight genes substantially in a *rectilinear band.* This strongly supports the linear hypothesis. Yet there remains the serious logical difficulty that the long distances were already long enough before we increased them by allowing for double crossing-over. When so increased they will of necessity be too long, since they will now exceed 50, the limiting value for cross-over percentages involving linkage. It must then be frankly recognized that map distances do not correspond with cross-over percentages (although they are based on them) except when the cross-over values are very low. This has been made clear by Haldane[7] who designates the map units "morgans" to distinguish them from the directly observed cross-over percentages. He gives a useful table for converting cross-over percentages into map-distances and vice versa. How widely the two may diverge is illustrated in the following table in which are shown the linkage relations of the gene, star, with other second chromosome genes.

	OBSERVED CROSS-OVER PERCENTAGE (TABLE 140, BRIDGES AND MORGAN)	LINEAR MAP DISTANCE (FIG. 72, BRIDGES AND MORGAN)
Star—streak	15.9	15.4
Star—dachs	Not given	29.0
Star—black	37.9	46.5
Star—purple	43.7	52.7
Star—vestigial	43.3	65.0
Star—curved	45.9	73.5
Star—plexus	46.7	96.2
Star—arc	Not given	98.4
Star—speck	Not given	105.1
Star—morula	Not given	106.3

It appears from the table that cross-over percentages, compared with map distances, increase very slowly after they have once become as high as 40. According to Haldane's table, the cross-over percentage would not attain 50 until the map-distance reaches infinity.

Has the model figured in this paper any value either to confirm or to disprove the linear hypothesis? It does not, like the models of chromosomes 1 and 3, show the genes in a curved band lying in one plane. But it does show them lying roughly in a linear chain winding cork-screw fashion through the model. If all wires over 40 inches long were cut, the system would straighten out so as to approach a linear arrangement. I conclude that the model supports the linear hypothesis, if it be supposed that the longer distances have been shortened by double crossing-over, and that map distances in such cases should exceed observed cross-over percentages.

[1] These PROCEEDINGS, **5,** 25, 32, and 500.

[2] *Carnegie Inst. Washington, Publ.* **237,** 1916.

[3] *Genetics,* **3,** 1918 (107–134).

[4] Bridges, C. B., and Morgan, T. H., "The Second Chromosome Group of Mutant Characters," *Carnegie Inst. Washington, Publ.* **278,** 1919 (123–304).

[5] Gowen, J. W., "A Biometrical Study of crossing Over." *Genetics,* **4**; May, 1919 (205–250).

[6] These PROCEEDINGS, **5,** May, 1919.

[7] Haldane, J. B. S., *Genetics,* **8,** Sept., 1919 (306).

THE DEVELOPMENT OF CONNECTIVE TISSUE IN THE AMPHIBIAN EMBRYO

BY GEORGE A. BAITSELL

OSBORN ZOÖLOGICAL LABORATORY, YALE UNIVERSITY

Communicated by R. G. Harrison. Read before the Academy, November 10, 1919

The researches[1] in which the author has been engaged for several years have shown, in brief, that the structure of the plasma clot of frog's blood is of such a nature that when influenced by the proper mechanical factors, e.g., tension or pressure, its structure will be radically changed. In cases of this kind a fusion and consolidation of the minute elements of the clot will take place and, as a result, long fibers will be formed which unite in wavy bundles, anastomose with other bundles and ramify in various directions throughout the clot, thus resulting in the formation of a material which, at least in its morphology, is like certain types of connective tissue. In wounds in frog's skin, the experiments showed that a fibrous tissue formed from a plasma clot functioned, at least temporarily, as a normal connective tissue and there was no evidence to show that it would ever be replaced.

The above results led naturally to the question as to whether a similar process normally takes place in the histogenesis of connective tissue in amphibian embryos. The results obtained from these investigations are as follows:

1. The primitive forerunner of connective tissue in frog embryos is an amorphous, gelatinous material which, because of the fact that it stains